

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

~~<120> MCH Receptor Antagonist~~

<130> Case2651

<150> JP 11-266278

<151> 1999-09-20

<150> JP 2000-221055

<151> 2000-07-17

<160> 16

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<212> DNA

<213> Artificial Sequence

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<213> Artificial Sequence

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<210> 3

<211> 353

<212> PRT

<213> Rat

<400> 3

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		20						25					30		
Thr	Gly	Ser	Val	Ser	Tyr	Ile	Asn	Ile	Ile	Met	Pro	Ser	Val	Phe	Gly
		35					40						45		
Thr	Ile	Cys	Leu	Leu	Gly	Ile	Val	Gly	Asn	Ser	Thr	Val	Ile	Phe	Ala
		50				55					60				
Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Ser	Asn	Val	Pro	Asp	Ile
65				70					75					80	
Phe	Ile	Ile	Asn	Leu	Ser	Val	Val	Asp	Leu	Leu	Phe	Leu	Leu	Gly	Met
			85						90					95	
Pro	Phe	Met	Ile	His	Gln	Leu	Met	Gly	Asn	Gly	Val	Trp	His	Phe	Gly
		100						105						110	
Glu	Thr	Met	Cys	Thr	Leu	Ile	Thr	Ala	Met	Asp	Ala	Asn	Ser	Gln	Phe
		115						120						125	
Thr	Ser	Thr	Tyr	Ile	Leu	Thr	Ala	Met	Thr	Ile	Asp	Arg	Tyr	Leu	Ala
		130						135						140	
Thr	Val	His	Pro	Ile	Ser	Ser	Thr	Lys	Phe	Arg	Lys	Pro	Ser	Met	Ala
145					150					155				160	
Thr	Leu	Val	Ile	Cys	Leu	Leu	Trp	Ala	Leu	Ser	Phe	Ile	Ser	Ile	Thr
				165						170				175	
Pro	Val	Trp	Leu	Tyr	Ala	Arg	Leu	Ile	Pro	Phe	Pro	Gly	Gly	Ala	Val
			180					185						190	
Gly	Cys	Gly	Ile	Arg	Leu	Pro	Asn	Pro	Asp	Thr	Asp	Leu	Tyr	Trp	Phe
		195						200						205	
Thr	Leu	Tyr	Gln	Phe	Phe	Leu	Ala	Phe	Ala	Leu	Pro	Phe	Val	Val	Ile
		210						215						220	

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
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Thr

$\langle 210 \rangle$ 4

<211> 1074

<212> DNA

<213> Rat

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ATCAACATCA	TTATGCCTTC	CGTGTTTGGT	ACCATCTGTC	TCCTGGGCAT	CGTGGGAAAC	180
TCCACGGTCA	TCTTTGCTGT	GGTGAAGAAG	TCCAAGCTAC	ACTGGTGCAG	CAACGTCCCC	240
GACATCTTCA	TCATCAACCT	CTCTGTGGTG	GATCTGCTCT	TCCTGCTGGG	CATGCCTTTC	300
ATGATCCACC	AGCTCATGGG	GAACGGCGTC	TGGCACTTTG	GGGAAACCAT	GTGCACCCCTC	360
ATCACAGCCA	TGGACGCCAA	CAGTCAGTTC	ACTAGCACCT	ACATCCTGAC	TGCCATGACC	420

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 ATGGCCACCC TGGTGATCTG CCTCCTGTGG GCGCTCTCCT TCATCAGTAT CACCCCTGTG 540
 TGGCTCTACG CCAGGCTCAT TCCCTTCCCA GGGGGTGCTG TGGGCTGTGG CATCCGCCTG 600
 CCAAACCCGG AACTGACCT CTA CTGGTTC ACTCTGTACC AGTTTTTCCT GGCCTTTGCC 660
 CTTCCGTTTG TGGTCATTAC CGCCGCATAC GTGAAAATAC TACAGCGCAT GACGTCTTCG 720
 GTGGCCCCAG CCTCCCAACG CAGCATCCGG CTTCGGACAA AGAGGGTGAC CCGCACGGCC 780
 ATTGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT GCAGCTGACC 840
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 TTGGGCTATG CTAACAGCTG CCTGAACCCC TTTGTGTACA TAGTGCTCTG TGAGACCTTT 960
 CGAAAACGCT TGGTGTTGTC AGTGAAGCCT GCAGCCCAGG GGCAGCTCCG CACGGTCAGC 1020
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<211> 262

<212> RNA

<213> Rat

<400> 5

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 AUCAGCUGUC UGAGCGUUGC UGACCGUGCG GAGCUGCCCC UGGGUCGCAG GCUUCACUGA 180
 CAACACCAAG CGUUUUCGAA AGGUCUCACA GAGCACUAUG UACACAAAGG GGUUCAGGCA 240
 GCUGUUAGCA UAGCCCAAGC UG 262

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<212> DNA

<213> Artificial Sequence

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<210> 7

<211> 18

<212> DNA

<213> Artificial Sequence

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<223>

<400> 7

CCTGGTGATC TGCCTCCT 18

<210> 8

<211> 1275

<212> DNA

<213> Human

<400> 8

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 GGACAAGGTG GCAGGCGCTG GAGGCTGCCG CAGCCTGCGT GGGTGGAGGG GAGCTCAGCT 180
 CGGTTGTGGG AGCAGGCGAC CGGCACTGGC TGGATGGACC TGGAAGCCTC GCTGCTGCCC 240
 ACTGGTCCCA ACGCCAGCAA CACCTCTGAT GGCCCCGATA ACCTCACTTC GGCAGGATCA 300
 CCTCCTCGCA CGGGGAGCAT CTCCTACATC AACATCATCA TGCCTTCGGT GTTCGGCACC 360
 ATCTGCCTCC TGGGCATCAT CGGGAAGTCC ACGGTCATCT TCGCGGTCGT GAAGAAGTCC 420
 AAGCTGCACT GGTGCAACAA CGTCCCCGAC ATCTTCATCA TCAACCTCTC GGTAGTAGAT 480
 CTCCTCTTTC TCCTGGGCAT GCCCTTCATG ATCCACCAGC TCATGGGCAA TGGGGTGTGG 540
 CACTTTGGGG AGACCATGTG CACCCTCATC ACGGCCATGG ATGCCAATAG TCAGTTCACC 600
 AGCACCTACA TCCTGACCGC CATGGCCATT GACCGCTACC TGGCCACTGT CCACCCCATC 660
 TCTTCCACGA AGTTCCGGAA GCCCTCTGTG GCCACCCTGG TGATCTGCCT CCTGTGGGCC 720
 CTCTCCTTCA TCAGCATCAC CCCTGTGTGG CTGTATGCCA GACTCATCCC CTTCCCAGGA 780
 GGTGCACTGG GCTGCGGCAT ACGCCTGCCC AAGCCAGACA CTGACCTCTA CTGGTTCACC 840
 CTGTACCAGT TTTTCCTGGC CTTTGCCCTG CCTTTTGTGG TCATCACAGC CGCATACGTG 900
 AGGATCCTGC AGCGCATGAC GTCCTCAGTG GCCCCGCCT CCCAGCGCAG CATCCGGCTG 960

CGGACAAAGA GGGTGACCCG CACAGCCATC GCCATCTGTC TGGTCTTCTT TGTGTGCTGG 1020
 GCACCCTACT ATGTGCTACA GCTGACCCAG TTGTCCATCA GCCGCCCAGAC CCTCACCTTT 1080
 GTCTACTTAT ACAATGCGGC CATCAGCTTG GGCTATGCCA ACAGCTGCCT CAACCCCTTT 1140
 GTGTACATCG TGCTCTGTGA GACGTTCCGC AAACGCTTGG TCCTGTCGGT GAAGCCTGCA 1200
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<210> 9

<211> 422

<212> PRT

<213> Human

<400> 9

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				20				25					30		
Cys	Gly	Ala	Cys	Ala	Pro	Gly	Gln	Gly	Gly	Arg	Arg	Trp	Arg	Leu	Pro
		35					40					45			
Gln	Pro	Ala	Trp	Val	Glu	Gly	Ser	Ser	Ala	Arg	Leu	Trp	Glu	Gln	Ala
	50					55				60					
Thr	Gly	Thr	Gly	Trp	MeT	Asp	Leu	Glu	Ala	Ser	Leu	Leu	Pro	Thr	Gly
65				70					75				80		
Pro	Asn	Ala	Ser	Asn	Thr	Ser	Asp	Gly	Pro	Asp	Asn	Leu	Thr	Ser	Ala
			85					90				95			
Gly	Ser	Pro	Pro	Arg	Thr	Gly	Ser	Ile	Ser	Tyr	Ile	Asn	Ile	Ile	MeT
		100					105					110			
Pro	Ser	Val	Phe	Gly	Thr	Ile	Cys	Leu	Leu	Gly	Ile	Ile	Gly	Asn	Ser
		115				120						125			
Thr	Val	Ile	Phe	Ala	Val	Val	Lys	Lys	Ser	Lys	Leu	His	Trp	Cys	Asn
	130					135						140			

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu			
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Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly			
	165	170	175
Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp			
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Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile			
	195	200	205
Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg			
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Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser			
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Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe			
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	260	265	270
Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu			
	275	280	285
Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met			
	290	295	300
Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr			
	305	310	315
Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val			
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Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser			
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Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu			
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Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys			

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Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln		
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<210> 11

<211> 31

<212> DNA

<213> Artificial Sequence

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<400> 11

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<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

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<223>

<400> 12

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<210> 13

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223>

<400> 13

AACTAGTTCA GGTGCCTTTG CTTTCTGTCC TCT 33

<210> 14

<211> 1074

<212> DNA

<213> Human

<400> 14

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 ATCAACATCA TCATGCCTTC GGTGTTCCGG ACCATCTGCC TCCTGGGCAT CATCGGGAAC 180
 TCCACGGTCA TCTTCGCGGT CGTGAAGAAG TCCAAGCTGC ACTGGTGCAA CAACGTCCCC 240
 GACATCTTCA TCATCAACCT CTCGGTAGTA GATCTCCTCT TTCTCCTGGG CATGCCCTTC 300
 ATGATCCACC AGCTCATGGG CAATGGGGTG TGGCACTTTG GGGAGACCAT GTGCACCCTC 360
 ATCACGGCCA TGGATGCCAA TAGTCAGTTC ACCAGCACCT ACATCCTGAC CGCCATGGCC 420
 ATTGACCGCT ACCTGGCCAC TGTCCACCCC ATCTCTTCCA CGAAGTTCCG GAAGCCCTCT 480
 GTGGCCACCC TGGTGATCTG CCTCCTGTGG GCCCTCTCCT TCATCAGCAT CACCCCTGTG 540
 TGGCTGTATG CCAGACTCAT CCCCTTCCCA GGAGGTGCAG TGGGCTGCGG CATA CGCCTG 600
 CCCAACCCAG AACTGACCT CTA CTGTTT ACCCTGTACC AGTTTTTCTT GGCCTTTGCC 660
 CTGCCTTTTG TGGTCATCAC AGCCGCATAC GTGAGGATCC TGCAGCGCAT GACGTCTCTA 720
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 ATCGCCATCT GTCTGGTCTT CTTTGTGTGC TGGGCACCCT ACTATGTGCT ACAGCTGACC 840

CAGTTGTCCA TCAGCCGCCC GACCCTCACC TTTGTCTACT TATACAATGC GGCCATCAGC 900
 TTGGGCTATG CCAACAGCTG CCTCAACCCC TTTGTGTACA TCGTGCTCTG TGAGACGTTT 960
 CGCAAACGCT TGGTCCTGTC GGTGAAGCCT GCAGCCCAGG GGCAGCTTCG CGCTGTCAGC 1020
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<211> 1283

<212> DNA

<213> Human

<400> 15

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 GGGACAAGGT GGCAGGCGCT GGAGGCTGCC GCAGCCTGCG TGGGTGGAGG GGAGCTCAGC 180
 TCGGTTGTGG GAGCAGGCGA CCGGCACTGG CTGGATGGAC CTGGAAGCCT CGCTGCTGCC 240
 CACTGGTCCC AACGCCAGCA ACACCTCTGA TGGCCCCGAT AACCTCACTT CGGCAGGATC 300
 ACCTCCTCGC ACGGGGAGCA TCTCCTACAT CAACATCATC ATGCCTTCGG TGTTCCGGCAC 360
 CATCTGCCTC CTGGGCATCA TCGGGAATC CACGGTCATC TTCGCGGTCG TGAAGAAGTC 420
 CAAGCTGCAC TGGTGCAACA ACGTCCCCGA CATCTTCATC ATCAACCTCT CGGTAGTAGA 480
 TCTCCTCTTT CTCCTGGGCA TGCCCTTCAT GATCCACCAG CTCATGGGCA ATGGGGTGTG 540
 GCACTTTGGG GAGACCATGT GCACCCTCAT CACGGCCATG GATGCCAATA GTCAGTTCAC 600
 CAGCACCTAC ATCCTGACCG CCATGGCCAT TGACCGCTAC CTGGCCACTG TCCACCCCAT 660
 CTCTTCCACG AAGTTCCGGA AGCCCTCTGT GGCCACCCTG GTGATCTGCC TCCTGTGGGC 720
 CCTCTCCTTC ATCAGCATCA CCCCTGTGTG GCTGTATGCC AGACTCATCC CCTTCCCAGG 780
 AGGTGCAGTG GGCTGCGGCA TACGCCTGCC CAACCCAGAC ACTGACCTCT ACTGGTTCAC 840
 CCTGTACCAG TTTTTCCTGG CCTTTGCCCT GCCTTTTGTG GTCATCACAG CCGCATACGT 900
 GAGGATCCTG CAGCGCATGA CGTCCTCAGT GGCCCCCGCC TCCCAGCGCA GCATCCGGCT 960
 GCGGACAAAG AGGGTGACCC GCACAGCCAT CGCCATCTGT CTGGTCTTCT TTGTGTGCTG 1020
 GGCACCCTAC TATGTGCTAC AGCTGACCCA GTTGTCCATC AGCCGCCCCGA CCCTCACCTT 1080
 TGTCTACTTA TACAATGCGG CCATCAGCTT GGGCTATGCC AACAGCTGCC TCAACCCCTT 1140
 TGTGTACATC GTGCTCTGTG AGACGTTCCG CAAACGCTTG GTCCTGTCGG TGAAGCCTGC 1200

AGCCCAGGGG CAGCTTCGCG CTGTCAGCAA CGCTCAGACG GCTGACGAGG AGAGGACAGA 1260
AAGCAAAGGC ACCTGAACTA GTT 1283

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<211> 420

<212> RNA

<213> Human

<400> 16

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GCUGCAGGCU UCACCGACAG GACCAAGCGU UUGCGGAACG UCUCACAGAG CACGAUGUAC 180
ACAAAGGGGU UGAGGCAGCU GUUGGCAUAG CCCAAGCUGA UGGCCGCAUU GUAUAAGUAG 240
ACAAAGGUGA GGGUCGGGCG GCUGAUGGAC AACUGGGUCA GCUGUAGCAC AUAGUAGGGU 300
GCCCAGCACA CAAAGAAGAC CAGACAGAUG GCGAUGGCUG UGCGGGUCAC CCUCUUUGUC 360
CGCAGCCGGA UGCUGCGCUG GGAGGCGGGG GCCACUGAGG ACGUCAUGCG CUGCAGGAUC 420